FIG. 1A

```
1    CTGCTTCCCACCAGCAAAGACCACGACTGGAGCCGGAGCCGGAGCTGGAAACATG       60
     ------+---------+---------+---------+---------+---------+
     GACGAAGGGGTCGTTTCTGGTGCTGACCTCTCGGCTCGGCCTCGACCCTTTGTAC
                                                            M

61   AAGAGCGTCTTGCTGCTGACCACGCTCCTCGTGCCTGCCCACCTGGTGGCCCTGGAGC    120
     ------+---------+---------+---------+---------+---------+
     TTCTCGCAGAACGACGACTGGTGCGAGGAGCACGGACGGGTGGACCACCGGGACCTCG
      K  S  V  L  L  L  T  T  L  L  V  P  A  H  L  V  A  A  W  S

121  AATAATTATGCGGTGGACTGCCCCTCAACACTGTGACAGCAGTGAGTCAAAAGCAGCCCG   180
     ------+---------+---------+---------+---------+---------+
     TTATTAATACGCCACCTGACGGGGAGTTGTGACACTGTCGTCACTCAGTTTTCGTCGGGC
      N  N  Y  A  V  D  C  P  Q  H  C  D  S  S  E  C  K  S  S  P

181  CGCTGCCAAGAGGACACAGTGCTCGACTGTGGCCGGACTGTGCCGAGTGTGCCGCAGGGCGG   240
     ------+---------+---------+---------+---------+---------+
     GCGACGGTTCCTGTGTCACGAGCTGACACCGGCCTGACACGGCTCACGCGGCGTCCCGCC
      R  C  K  R  T  V  L  D  D  C  G  C  C  R  V  C  A  A  G  R
```

MATCH WITH FIG. 1B

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FIG. 1B

MATCH WITH FIG. 1A

```
                                                                    300
241   GGAGAACTTGCTACCGCCACAGTCTCCAGGCATGATGGCATGAAGTGTGGCCCGGGGCTG
      ------+---------+---------+---------+---------+---------+
      CCTCTTGAACGATGGCGTGTCAGAGTCCGTACTTCACCGGGCCCCGAC
       G  E  T  C  Y  R  T  V  S  G  M  D  G  M  K  C  G  P  G  L

                                                                    360
301   AGGTGTCAGCCCTTCTAATGGGGAGGATCCCTTTGGTGAAGAGTTTGGTATCTGCAAAGAC
      ------+---------+---------+---------+---------+---------+
      TCCACAGTCGGAAGATTACCCCTCCCTAGGAAAACCACTTCTCAAACCATAGACGTTTCTG
       R  C  Q  P  S  N  G  E  D  P  F  G  E  E  F  G  I  C  K  D

                                                                    420
361   TGTCCCTACGGCACCTTCGGGGATGGATTGCAGAGAGACCTGCAACTGCCAGTCAGGCATC
      ------+---------+---------+---------+---------+---------+
      ACAGGGATGCCGTGGAAGCCCTACCTAACGTCTCTGGACGTTGACGGTCAGTCCGTAG
       C  P  Y  G  T  F  G  M  D  C  R  E  T  C  N  C  Q  S  G  I

                                                                    480
421   TGTGACAGGGGGACGGGGAAAATGCCTGAAATTCCCTTCTTCCAATATTCAGTAACCAAG
      ------+---------+---------+---------+---------+---------+
      ACACTGTCCCCTGCCCCTTTACGGACTTTAAGGGGAAGAAGGTTATAAGTCATTGGTTC
       C  D  R  G  T  G  K  C  L  K  F  F  F  F  Q  Y  S  V  T  K
```

MATCH WITH FIG. 1C

FIG. 1C

MATCH WITH FIG. 1B

```
481  TCTTCCAACAGATTTGTTCTCTCACGGAGCATCTGGAGATGGCAATATT
          --------+---------+---------+---------+---------+   540
     AGAAGGTTGTCTAAACAAAGAGAGAGTGCCTCGTAGACCTCTACCGTTATAA
      S  S  N  R  F  V  S  L  T  E  H  D  M  A  S  G  D  G  N  I

541  GTGAGAGAAGAAGTTGTGAAAGAGAATGCTGCCGGGTCTCCCGTAATGAGGAAATGGTTA
          --------+---------+---------+---------+---------+   600
     CACTCTCTTCTTCAACACTTTCTTACGACGGCCCAGAGGGCATTACTCCTTACCAAT
      V  R  E  E  V  V  K  E  N  A  A  G  S  P  V  M  R  K  W  L

601  AATCCACGCTGATCCCGGCTGTGATTTCTGAGAGAAGGCTCTATTTCGTGAYTGTTCAA
          --------+---------+---------+---------+---------+   660
     TTAGGTGCGACTAGGGCCGACACTAAAGACTCTTCCGAGATAAAGCACTRACAGTT
      N  P  R  *

661  CACACAGCCAACACATTTAGGAACTTTCTAGATTATAGCATAAGGACATGTAATTTTGAA
          --------+---------+---------+---------+---------+   720
     GTGTGTCGGTGTAAAATCCTTGAAAGATCTAATATCGTATTCCTGTACATTAAAAACTT

721  GACCAAATGTGATGCATGGTGATCCAGAAAAACAAAAGTAGGATACTTACAATCCATAA
          --------+---------+---------+---------+---------+   780
     CTGGTTACACTACGTACCACCTAGGTCTTTTGTTTTTCATCCTATGAATGTTAGGTATT
```

MATCH WITH FIG. 1D

FIG. 1D

MATCH WITH FIG. 1C

```
781 CATCCCATATGACTGAACACTTGTATGTGTTGTTGTTAAATATTCGAATGCATGTAGATTTGT    840
        ----+----+----+----+----+----+
    GTAGGTATACTGACTTGTGAACATACACAACAATTTATAAGCTTACGTACATCTAAACA
```

```
841 TAAATGTGTGTGTATAGTAACACTGAAGAACTAAAAATGCAATTAGGTAATCTTACATG    900
        ----+----+----+----+----+----+
    ATTTACACACACATATCATTGTGACTTCTTGATTTTTACGTTAAATCCATTAGAATGTAC
```

```
901 GAGACAGGTCAACCAAAGAGGGAGCTAGGCAAAGCTGAAGACCGCAGTGAGTCAAATTAG    960
        ----+----+----+----+----+----+
    CTCTGTCCAGTTGGTTCTCCCTCGATCCGTTCGACTTCTGGCGTCACTCAGTTTAATC
```

```
961 TTCTTTGACTTTGATGTACATTAATGTTGGGATATGGAATGAAGACTTAAGAGCAGGAGA    1020
        ----+----+----+----+----+----+
    AAGAAACTGAAACTACATGTAATTACAACCCTATACCTTACTTCTGAATTCTCGTCCTCT
```

```
1021 AGATGGGGAGGGGGTGGGAGTGGGAAATAAAATATTTAGCCCTTCCTTGGTAGGTAGCTT    1080
         ----+----+----+----+----+----+
     TCTACCCCTCCCCCACCCTCACCCTTTATTTTATAAATCGGGAAGGAACCATCCATCGAA
```

MATCH WITH FIG. 1E

FIG. IE

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MATCH WITH FIG. 1D

```
1081   CTCTAGAATTTAATTRTGCTTTTTTTTTTTTTTTTGGGCTTTGGGAAAAGTCAAAATAAA   1140
       --------+---------+---------+---------+---------+---------+
       GAGATCTTAAATTAAYACGAAAAAAAAAAACCCGAAACCCTTTCAGTTTTATTT

1141   ACAACCAGAAAACCCCTGAAGGAAGTAAGATGTTTGAAGCTTATGGAAATTTGAGTAACA   1200
       --------+---------+---------+---------+---------+---------+
       TGTTGGTCTTTGGGGACTTCCTTCATTCTACAAACTTCGAATACCTTAAACTCATTGT

1201   AACAGCTTTGANCTGAGAGCAATTYCAAAAGGCTGCTGATGTAGCCCCCGGGTTNCCTNT   1260
       --------+---------+---------+---------+---------+---------+
       TTGTCGAAACTNGACTCTCGTAARGTTTCCGACGACTACATCGGGGGCCCAANGGANA

1261   NTCTNAAGGAC   1271
       --------+--
       NAGANTTCCTG
```

```
                      1                                                      50
ce10_chick    ...MGSAGAR  P.ALAAALLC  LARLALGSPC  PAV....CQC  ...PAA.APQ
cyr6_mouse    ...MSSSTFR  TLAVAVTLAH  LTRLAL.STC  PAA....CHC  ...PLE.APK
ctgf_human    .MTAASMGPV  RVAFVVLLAL  CSRPAVGQNC  SGP....CRC  ...PDEPAPR
fisp-12       .MLASVAGPI  SLAL.VLLAL  CTRTATGQDC  SAQ....CQC  ...AAEAAPH
nov_chick     .METGGGQGL  PVLLLLLLL   RPCEVSGREA  ACPRPCGGRC  ...PAEP.PR
ibp_3human    MQRARPTLWA  AALTLLVLLR  GPPVARAGAS  SGGLGPVVRC  EPCVARALAR
ccn-4         .......MK   SVLLTTLLV   PAHLVAAWSN  MYAVDCPQHC  DSSECKSSPR
              .........   .........   .........   .........   .........

                      51                                                    100
ce10_chick    CAPGVGLVP.  ....DGCGCC  KVCAKQLNED  C....SRTQP  CDHTKGLECN
cyr6_mouse    CAPGVGLVR.  ....DGCGCC  KVCAKQLNED  C....SKTQP  CDHTKGLECN
ctgf_human    CPAGVSLVL.  ....DGCGCC  RVCAKQLGEL  C....TERDP  CDPHKGLFCD
              .........   .........   .........   .........   .........

                      401         411
ce10_chick    RLVNDIHKFR  D
cyr6_mouse    SLFNDIHKFR  D
ctgf_human    YYRKMYGDMA  .
fisp-12       YYRKMYGDMA  .
nov_chick     DPMSSEAKI.  .
ibp3_human    .........   .
ccn-4         .........   .
```

F I G. 2